

pgn1

1 GTCGAGGCAGTCACCTAACATGAAGTTTGACGAGGAGCCCAACTATGGGAAGCTTATTTCTCTTTTCGAT 69  
3 52 66  
50

HindIII  
AluI  
TaqI

70 ACTCTAATTGAGCCGTGCGCTCTATCTAGACCAATTAGCAATTGATGGAGCTCTAAAGTTGCTGGCTGT 138  
89 95 119 121

HhaI XbaI  
SacI  
AluI

139 TTTCTTGTTCATATGATTAACTTCTAAACTTGTGTATATAAATATTCTCTGAAAAGTGCTTTTGGCATA 207  
150 206

NdeI

208 TGTAGGTTGGGCAAAACGAGGAAGATTGCTTCTCAATTGGAAGATGATGAACAGCCGAGAGAGAAA 276

Sau3AI  
DdeI

277 TAAGAATAGGCAGTCCTGCTACTCAATGGATCTCAGTCTATAAAGGTCGTGCTGCCCATGAACAGAGGT 345  
309 305

FIG. 1A

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09782130 . 102202

EcRV  
346 AACACATTTTGGCATATACACTTTCATAGTTCCCTCACTAACTGTGTAATCTTTTGGTAGATATCACTA 414  
408  
415 CAATGTTGCAGAGACAANGCTGCGCJRRCATATACAGAAAGGGAATGAAGATGGCCCTTTTGATTAGCTG 483  
481  
469  
440  
440  
441  
434 439  
AluI HhaI  
NaeI  
MspI  
HpaII  
HaeIII  
AluI  
498  
484 TGTAGCATCAGCAGCTAAATCTCTGGGCTCTCATCATGGATGCTGGAACTGGATTCACTTCTCAAGTTTA 552  
535  
HinfI  
564  
564  
564  
553 TGAGTTGTCACCGGTCTTCCTACACAAGGTAATAATCAGTTGAAGCAATTAAGAATCAATCTGATTGT 621  
606  
DdeI  
622 AGTAACTAAGAGAAGAACTTACCTTAATGATTTCCTCCCGCAGGACTGGATTATGGAACAATGGGAAAGAAGAC 690  
629

FIG. 1B

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SacI  
691 TACTATATAAGCTCCATAGCGGTTTCAGATAACGGAGCTCTCTTTAGTTGTTATGTCAAAAAGGTTAGTGT 759  
AluI 702 729 731  
760 TTAGTGAATAAATAACTTATTATCAAAAAGTCTTCATTGACTTATTATATATACTTGTGTGAATTGGTA 828  
AluI  
829 GGAACCTACTTATTCTCAGCAGTCATACAAAGTGAGTGACTCATTTCCATTCAAGTGGATAAAATAAGAAA 897  
DdeI HinfI 866  
XmnI 843  
898 TGGAAAGAAGATTTTCATGTAACTCCCATGACAACCTGCTGGTAATCGTTGGGGTGTGGTAATGTCGAGG 966  
XmnI 909 TaqI 962  
Sau3AI  
BclI 982 982  
967 AACTCTGGCTTCTCTGATCAGGTAGGTTTTTTGTCTCTTATTGCTGTGCTGTTTTTATTTTCCCTGATAG 1035  
AluI  
1036 TCTAATATGATAAACTCTGCGTTGTGAAAGGTGGTGGAGCTTTGACTTTTGTACCCCAAGCGATGGGATA 1104  
AluI 1075 1088 RsaI

FIG. 1C

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09782130 102202

1105 CATAGGAGGTGGGATATAGATAACATCAATGGCAGCAACTGCGGATCAAGCAGCTTTTCATA 1173  
Sau3AI AluI  
1156 1166

1174 TTAAGCATACCAAAGCGTAAGATGGTGGATGAAACTCAAGAGACTCTCCGCACCCAGCGCTTTCCAAAGT 1242  
HinfI  
1216

1243 ACTCATGTCAAGGTTGGTTCTTTAGCTTTGAACACAGATTTGGATCTTTTGTGTTTCCATATAC 1311  
ScaI AluI Sau3AI  
RsaI  
1243 1269 1286

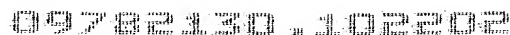
1312 ATAGGACCTGAGAGCTTTTGGTTGAATTTTTTTTTTTCAGGACAAATGGCGAAGAAATCTGTACATTG 1380  
DdeI AvaII AluI HinfI RsaI  
1316 1326 1368 1375

1381 CATCAATATGCTATGGCAGGACAGTGTGCTGATGATACACACTTAAGCATCATGTGTGTTAGAAAG 1449

1450 CCGAAGACAATTGGAGCGGAGCCCTCAGGGTGTGTCATAATACCAATCAAAGACGTAAACCAGACGAGTC 1518  
MstII DdeI Tth111I  
1472 1472 1514

FIG. 1D

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1933 TTTTTTGAATAATATCGTTTCATAAGATGTCACGCCAGGACATGAGCTACACATCACAATATTAGCATGCA 2001  
1968 1978 SphI  
BstNI AluI

2002 GATCGGACGATTGTCACTCACTTCAAAACACCTAAAGAGCTTCTCTCTCACAGCACACACATATG 2070  
2043 NdeI  
AluI

2071 CATGCAATATTTACACGTGATCGCCCATGCAAAATCTCCATTCTCACCTATAAAATTAGAGGCTCGGCTTCA 2139  
2073 2075 SphI  
NsiI Sau3AI

2140 CTTTTTACTCAAAACCAAACTCATCACTACAAACATACACAATGGCGAACAAGCTCTTC 2200  
2195 Met  
AluI

FIG. 1F

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Lambda CGNI-2  
NCG-186 Linear Length = 4325

XhoI  
TaqI  
AvaI  
||  
CTCGAGGCGAGTCACTAACATGAAGTTTGACGAGGAGGCCCAACTATGGGAAGCTTATTTCTCTTTTCGAT  
2 3 66  
50  
HindIII  
AluI  
|  
TaqI  
69

ACTCTAATTGAGCCGTGCGCTCTATCTAGACCAATTAGAATTGATGGAGCTCTAAAGGTTGCTGGCTGT 138  
89 95 119 121  
HhaI XbaI  
SacI  
AluI  
|  
NdeI  
150  
TTTCTTGTTTCATATGATTAACCTTCTAAACTTGTGTATAAAATATTCTCTGAAAGTGCTTTTGGCATA 206  
207  
TGTAGGTTGGGCAAAACGAGGAAGATTGCTTCTCAATTGGAAGAGGATGAACAGCGCAAGAGAAA 276  
Sau3AI  
DdeI  
|  
TAAGAATAGGCAGTCCTGCTACTCAATGGATCTCAGTCTATATAACGGTCGTCGCCATGAACAGAGGT 345  
309 305  
EcoRV  
414  
AAAACATTTTGTGCATATACACTTTGAAGTTCCTCACTAACTGTGTAATCTTTTGGTAGATATCACTA

FIGURE 2A

408

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007021301 1022002

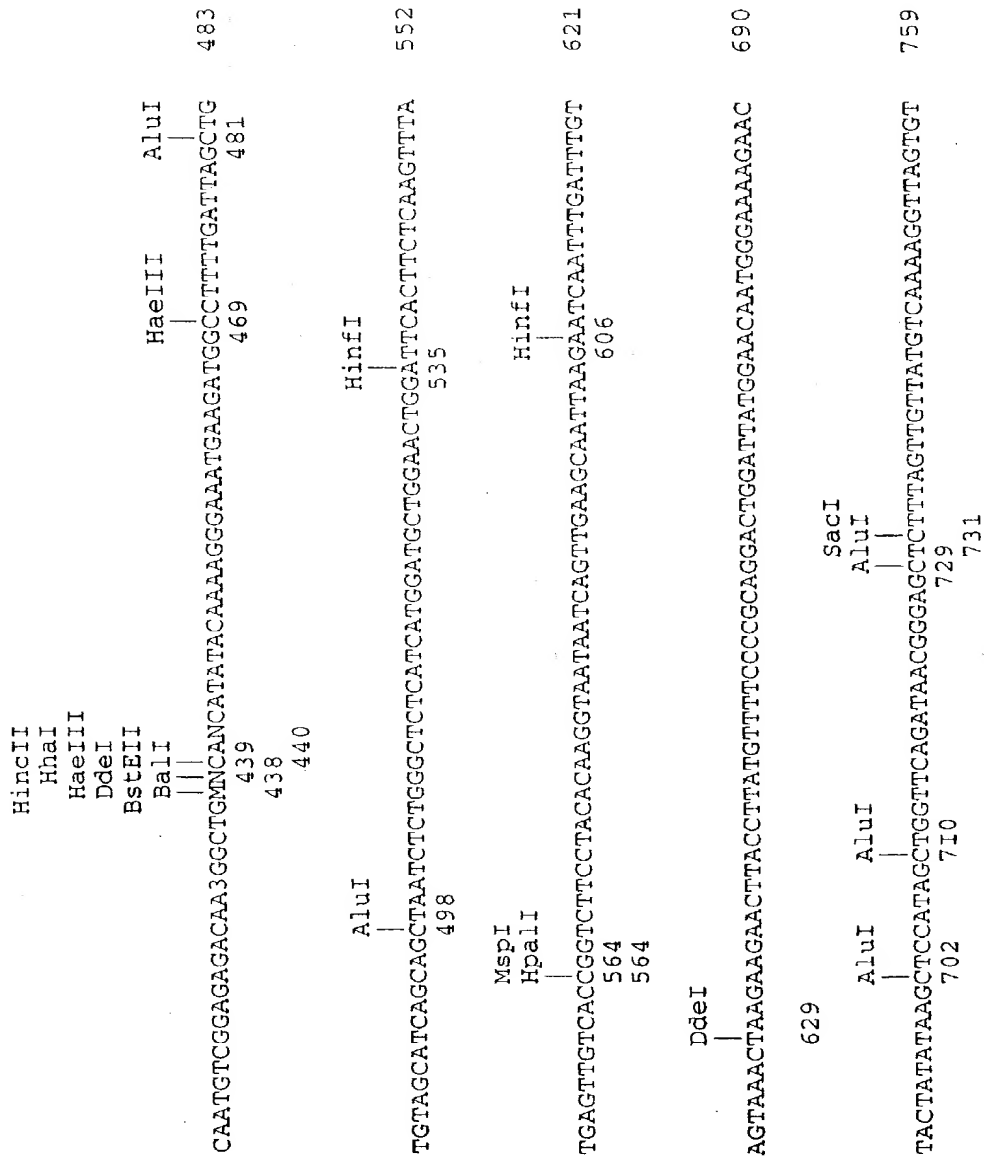


FIGURE 2B

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09782130 1022002

TTAGTGAATAAATACTTATACCAAAAGCTTTCATTGACTTATTTATATATACTTGTGTGAATTGCTAG 828

DdeI | HinfI

GAACTACTTATTTCTCAGCAGTCATACAAAAGTGAGTGACTCATTTCCGTTCAAGTGGATAAATAAGAAAT 897

842 865

XmnI | TaqI

GCAAAGAAGATTTTTCATGTAAACCTCCATGACAACTGCTGGTAATCGTTGGGTGTGGTAATGTTCGAGGA 966

908 961

Sau3AI | BclI

ACTCTGGCTTCTCTGATCAGGTAGGTTTTTGTCTCTTATTGTCTGGTGTGTTTTTATTTTCCCTGATAGT 1035

981

AluI | RsaI

CTAATATGATAAACTCTCGGTTGTGAAAAGGTGGTGGAGCTTTGACTTTTGTACCCAAAGCGATGGGATAC 1104

1074 1087

Sau3AI | AluI

ATAGCAGGTGGGAGAAATGGGTATAGAAATAACATCAATGGCAGCAACTGGGGATCAAGCAGCTTTTCATAT 1173

1155 1165

HinfI | ScaI

TAAGCATACCAAGCGTAAGATGGTGGATGAAACTCAAGAGACTCTCCGCCACCACCGCTTTTCCAAGTA 1242

1215 1242

RsaI

FIGURE 2C

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CTCATGTC AAGGTTGGTTCTTTAGCTTTTGAACACAGATTGGATCTTTTGGTTTGTGTTTCCATATACT 1311  
 1268 1285 1311 DdeI  
 AluI Sau3AI  
 TAGGACCTGAGAGCTTTTGGTTGATTTTTCAGGACAAATGGCGGAAGAATCTGTACATTGCATCA 1380  
 1315 1325 1363 1370 HinfI RsaI  
 DdeI  
 AuaI AluI  
 ATATGCTATGGCAGGACAGTGCTGTATACACACTTAAGCATCATGTGGAAGCCAAAGACAATTGGAG 1449  
 HinfI  
 DdeI  
 CGAGACTCAGGTCGTCATAATAACCAATCAAGACGTTAAACCCAGACGCAACCTCTTTGGTTGAATGTA 1518  
 1456 1454 RsaI  
 ATGAAAGGGATGTGCTCTGGTATGTATGTACGAATAACAAAGAGAGAGATGGAATTAGTAGAATAA 1587  
 1548  
 AluI EcoRV  
 TTTGGGAGCTTTTAAAGCCCTTCAAGTGTGCTTTTATCTTATTCATATCATCCATTGCGTTGTTAA 1656  
 1596 1635  
 XbaI DdeI  
 TCGCTCTCTAGATATGTTCCCTATATCTTTCTCAGTGTCTGTATAAGTGAATGTGAGAAAACCATACCAA 1725  
 1664 1687

FIGURE 2D

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Hinfi  
ACCAAAATATTCAAATCTTATTTTAAATGTTGAATCACTCGGAGTTGCCACCTTCTGTGCCAATIG 1794  
1761  
HinfI  
TGCTGAATCTATCACACTAGAAAAAACATTTCTTCAAGGTAATGACTTGTGGACTATGTTCTGAATTC 1863  
1800  
EcoRI  
TCATTAAAGTTTATTTTCTGAAGTTTAAAGTTTACCTTCTGTTTGAATATATATCGTTTCATAAGATG 1932  
SphI  
BstNI AluI  
1940 1950  
SphI  
Sau3AI  
1971  
TACAGCCAGGACATGAGCTACACATCGCACATAGCATGCAGATCAGGACGATTGTGTCACCTCACTTCAAA 2001  
1973  
DdeI AluI HhaI NdeI SphI  
2006 2012 2028 2036 2042 2044  
Sau3AI  
2058  
CACCTAAGAGCTTCTCTCTCACAGCGCACACACATATGCATGCCAATATTTACACGTTGATCGCCCATGCCAA 2070  
ATCTCCATTCTCACCTATAAATTAGAGCCTCGGCTTCACTCTTTACTCAAAACCAAACTCATCTACA 2139  
AluI  
2164  
GAACATACACAAATGGCGAACAAAGCTCTTCTCGTCTCGGCAACTCTCGCCTTGTCTTCTTCTCACC 2208  
MetAlaAsnLysLeuPheLeuValSerAlaThrLeuAlaLeuPheLeuLeuThr

FIGURE 2E

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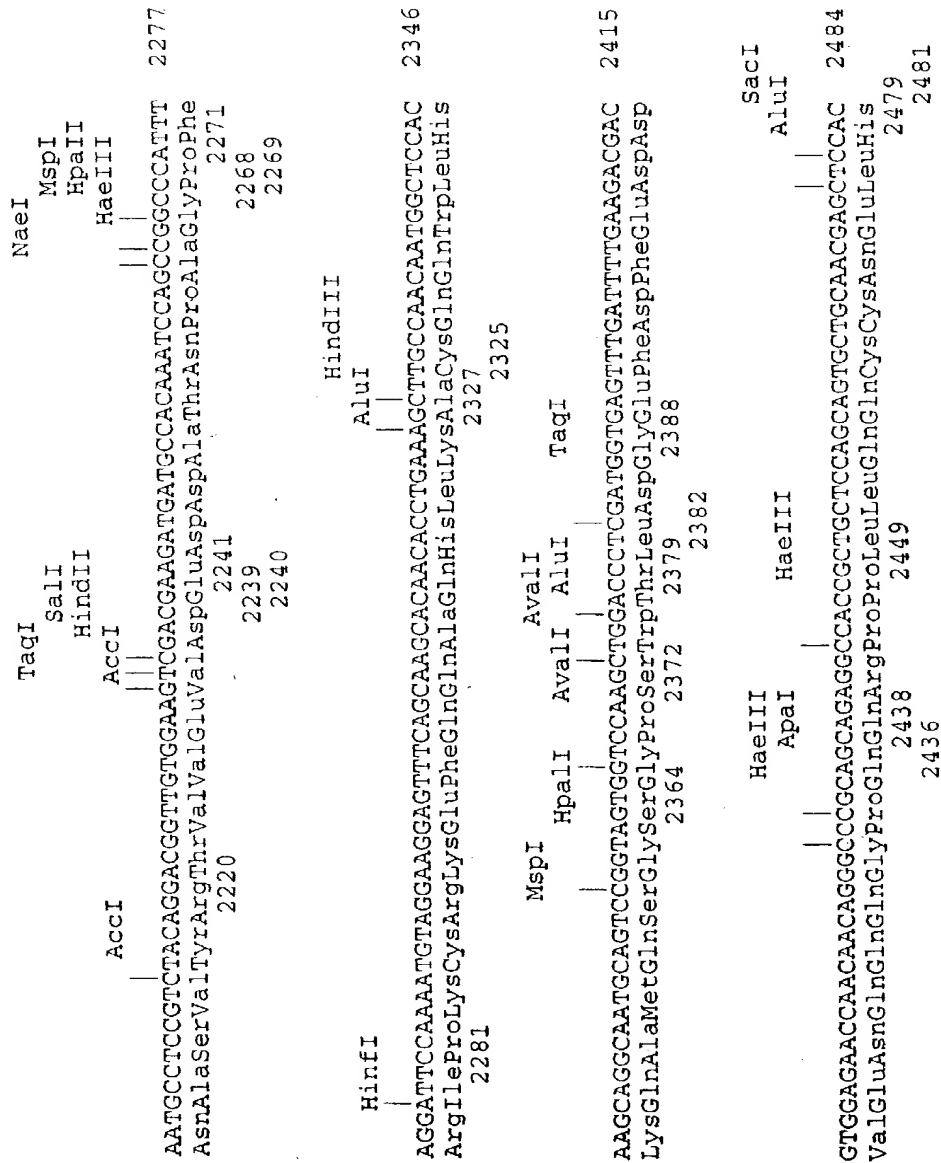


FIGURE 2F

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2553  
TaqI  
HinfI  
BstNI  
2486  
2548  
2551  
2622  
2639  
2688  
2760  
2736  
2724  
2725  
2707  
2694  
2692

CAAGGAAGAGCCACTTTGCGTTTCCCCAACCTTGAAGGAGCATCCAAAGCCGTTAAACAACAGATTCTGA  
GlnGluGluProLeuCysValCysProThrLeuLysGlyAlaSerLysAlaValLysGlnGlnIleArg  
2486  
2548  
2551  
2622  
2639  
2688  
2760  
2736  
2724  
2725  
2707  
2694  
2692

CAACAACAGGGACAAACAATGCAGGGACAGCAGATGCAGCAAGTGATTAGCCGTATCTACCAGACCCGCT  
GlnGlnGlnGlyGlnMetGlnGlnMetGlnGlnMetGlnGlnValIleSerArgIleTyrGlnThrAla  
2622  
2639  
2688  
2760  
2736  
2724  
2725  
2707  
2694  
2692

ACGCACCTACCTAGAGCTTGCAACATCAGGCAAGTTAGCATTTGCCCTTCCAGAGACCATGCCCTGGG  
ThrHisLeuProArgAlaCysAsnIleArgGlnValSerIleCysPropheGlnLysThrMetProGly  
2639  
2688  
2760  
2736  
2724  
2725  
2707  
2694  
2692

MspI  
HpaII  
HaeIII  
ApaI  
XhoI  
TaqI  
AvaI  
HinfI  
AccI

FIGURE 2G

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HindII		RsaI	
GTTGATGATATGTTAACACACTACATAGTCATGGTGTGTGTTCCATATAAATAATGTACTAATGTAATAAGAAC			2829
2771		2813	
AccI			
TACTCCGTAGACGGTAATAAAAAGAGAAAGTTTTTTTTTTTACTCTTGCTACTTTCCTATATAAAGTGATGAT			2898
2838			
		ScaI	
		RsaI	
TAACAACAGATACACCAAAAAGAAAAACAATTAAATCTATATTCCACAATGAAGCAGTACTAGTCTATTGAA			2967
		2954	
		Sau3AI	
CATGTCAGATTTTCTTTTCTTAAATGTCTAATTAAGCCTTCAAGGCTAGTGTGATGATAAAAGATCATCCA			3036
		3028	
Sau3AI			
BamHI	HinfI		
ATGGGATCCAACAAGACTCAAAATCTGGTTTTTGATCAGATACTTCAAAAACACTATTTTGTATTTCATTAA			3105
3041	3053		
	3069		

**FIGURE 2H**

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HinfI  
TTATGCAAGTGTCTCTTTATTTGGTGAAGACTCTTTAGAGCAAAACAACGACAAGCAGTAATAAAAAA 3174  
3135  
ACAAAGTTCAGTTTAAAGATTGTTATTGACTTATTGCTATTGCAATTGCAAAAAATATAGTATGATATTATATA 3243  
GTTTTATTATATAATGCTTGTCTATTCAAGATTGAGAACATTAATATGATACGTCCACATATCCAA 3312  
NdeI  
TATATTAAGTTTCATTTCTGTTCAAAACATATGATAAGATGGTCAAAATGATTATGAGTTTGTATTAC 3381  
3341  
TaqI      Sau3AI  
AluI      RsaI  
CTGAAGAAAAGATAAGTGAGCTTTCGAGTTTCTGAAGGGTACGTGATCTTTCATTTCTTGGCTAAAAGCGA 3450  
3402      3421      3425  
ATATGACATCACCTAGAGAAAGCCGATAATAGTAAACTCTGTTCTTGGTTTTTGGTTTAAATCAAACCGA 3519  
MspI      DdeI  
HpaI      AluI      NdeI      HinfI      MspI      HpaI  
ACCGGTAGCTGAGTGTCAAGTCAGCAAAACATCCGAAACCATATGTCAATTCGTTAGATTCCCGGTTAA 3588  
3522      3528      3560      3576      3581  
3529

FIGURE 2I

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Mspl  
HpalI  
|  
GTTGTAAACCGGTATTTTCATTGGTGAAACCCCTAGAACCCAGCCAGCCANCCCTTTTAAATCTAATTTTGCA 3657  
3598

HinfI  
HincII  
|  
DdeI  
|  
BstNI  
|  
AACGAGAAGTCACCAACCTCTCCACTAAACCCCTGAACCTTACTGAGAGAAGCCAGAGNCANNAAGAA 3726  
3702 3718  
3715  
3714

AvaiI  
AluI  
|  
CGGCGG5MNTTGTGGCGGCGGCGGACGTTTTTGGTGGCGGCGGTGGACGTTTTTGGTGGCGGCGGCGGTGCA 3864  
3804  
3801

EcoRV  
|  
AvaiI  
|  
DdeI  
|  
CCTTTGGTGGGATATCGTGACGAAGGACCTCCACGTGAAGTCATTGGTTGTTTACTCTTTCTTAG 3933  
3880 3892 3930

FIGURE 2J

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3935  
3937  
3974  
3976  
4000  
4002  
4004  
4023  
4059  
4069  
4071  
4085  
4140  
4146  
4209  
4210  
4217  
4222  
4231  
4278

TaqI  
HinfI  
HindIII  
AluI  
DdeI

TCGAATCTTATTCTTGCTCTGCTCGTTGTTTACCGATAAAAGCTTAAGACTTTATTGATAAAGTTCTCA

AluI  
XmnI  
HinfI  
DdeI

GCTTTGAATGTGAATGAACGTGTTTCCCTGCTTATTAGTGTTCCCTTTGTTTGGAGTTGAATCACTGTCTTA

HincII

GCACCTTTGTGATTCATCTTTGTGTTTAAAGTTAAAGGTAGAAACTTTGTGACTTGTCTCCGTTATG

HincII

ACAAGGTTAACTTTGTTGGTTATAACAGAAAGTTGCGACCTTTCTCCATGCTTGTGAGGGTGATGCTGTG

AvaI  
AluI  
DdeI  
Sau3AI

GACCAAGCTCTCTCAGCGGAAGATCCCTTACTTCAATGCCCCCAATCTACTTGGAAAACAAGACACAGAT

FIGURE 2K

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TaqI  
 SalI  
 PstI  
 HindIII  
 Sau3AI  
 AluI  
 AccI  
 EcoRI  
 TCGGAAAGTTGATGAGATCCAGCTTGGGCTGCAGGTCGACGAATTC  
 4294 4302 4316 4321  
 4300 4314 4313 4315

4325

FIGURE 2L

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*Brassica campestris* ACP Genomic Sequence

1 AAGAGTATGCTACTACTACTACTCTCTATAATCAAGTTTCAAGAAGCTGAGCTTGGCTCTCACTTTATAT 69  
11 46 51  
47  
70 GTTTGATGTTGTTGTCAGGATGGTAAATCATGGAAGAGATAAAGAATGCAAAACCTGAAGTATTGG 138  
139 CAGAGAGGACTGAGGTGAGAGAGCATGTCACCTTTTGTGTTACTCATCTGAATTATCTTATATGCCAATT 207  
149  
208 GTAAAGTGGTACTAAAAGGTTTGTAACTTTTGGTAGGTGGATTTGAAGGATAAATGGAGGAACCTTGCTTC 276  
217  
277 GGTAGCGGTAACAAGTTTTATATTGCTATGAAGCTTTTTCCTGCGTGACGTATCAGCAGCTGTGGAG 345  
310 338 338  
308

AccI |  
DdeI |  
AluI |  
AluI |  
HindIII |  
AluI |  
PvuII |  
AluI |

FIGURE 3A

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346 AAGATGGTATTAGAAAGGGTCTTTTTCACATTTTGTGTGTGTGACAAAATATAATTCCGCCCGGTATGGTTT 414  
MspI  
HpaII  
HaeIII  
403  
404  
404

415 GGTTAAGACTTGTTGAGAGACGCTGTGGGGTTTTTTTGATGTATAATTAGTCGTGTGTGTAGAACGAAACAA 483

484 GACTTGTTGNGTATGCTTTTTTTTAACTGAGGGGTTTGTGTGTGTGTAGTTAGGAACCTTGACTTTGTCT 552  
Tth1111I  
547

553 CTTTCTCTCAAGATCTGATTGGTAAGGCTCTGGGTGGTAGTACTGTTTGGTTTAAATTTGTTTGTACTATT 621  
ScaI  
RsaI  
564  
564  
593  
593

622 GAGTCACTGTGGCCCATTTGACTTTTAAATTAGGCTGGTATATTTTTTTTGGTTTAAACCGGTCTCAGATAG 690  
HinfI  
HaeIII  
DraI  
HpaII  
DraI  
MspI  
DdeI  
623  
634  
646  
673  
678  
683  
678

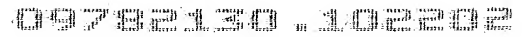
FIGURE 3B

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**FIGURE 3C**

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HaeIII HindIII  
AluI  
967 AAGGCCCATGTTATCATAAAACGCCGTCGTTTTCAGTGCACCAAGCTTATAAATGTAGCCAGCTACCTC 1035  
971 1012 1029 1034  
1010  
XhoI  
RsaI  
Tth1111  
TaqI  
Sali  
HincII  
AccI  
1036 GGGACATCAGCGCTCTTTGTACACTCCGCCCATCTCTCTCTCTCGAGCAGATCTCTCTCGGGAATATCG 1104  
1078 1085 1093 1103  
1079 1085  
1078  
TaqI  
AvaI  
BglII  
Sau3AI  
AvaI  
1105 ACAATGTCGACCACTTTCTGCTCTTCCGTCCTCCATGCCAAGCCACTTCTCTGTGTAATCTCATCTCCTTCT 1173  
1112  
1110  
1111  
1112  
1108  
METSerThrThrPheCysSerSerValSerMETGlnAlaThrSerLeu

FIGURE 3D

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03781110.142202

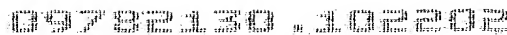
1174 TGTGTTCCAGATCGCTCTGATCATACACTTCTTTTAGATCATTTGGCCTCTGATCTGTGCTTGATGTTT 1242  
Sau3AI BclI Sau3AI  
1184 1193 1210 1224  
1193  
HincII AluI HinfI  
1243 GTTAACCTCTCCACGCATGTTTGATTATGTTGAGAAATTAGAAAAAATGTTAGCTTTACGAAATCTTTAG 1311  
1243 1296 1303  
Sau3AI TaqI Sau3AI  
1312 TGATCATTTCAATTGGATTGCAATCTTGTGTGACATTTGAGGCTTGTGTAGATTTCCGATCTGTATTCA 1380  
1313 1369  
1313 1368  
HinfI AluI DraI  
1381 TTTTGAATCACAGCTATAATAGTCATTTGAGTAGTAGTGTGTTTTTAAATGAACATGTTTGTGTATTGA 1449  
1386 1394 1425  
AluI  
1450 TGGACAAACAGGCAGCAACAACGAGGATTAGTTTCCAGAAGCCAGCTTTGGTTTCAACGACTAATCTC 1518  
AlaAlaThrThrArgIleSerPheGlnLysProAlaLeuValSerThrThrAsnLeu  
1496

FIGURE 3E

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**FIGURE 3F**

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1864 GTGATGGGTTTAGAGGAAGAGTTTGATATCGAAATGGCTGAAGAGAAAGCTCAGAAGATTGCTACTGTG 1932  
ValMetGlyLeuGluGluGluPheAspIleGluMetAlaGluGluLysAlaGlnLysIleAlaThrVal  
1891 1893 1914 1914  
1893  
1933 GAGGAAGCTGCTGAACCTCATTGAAGAGCTCGTTCAACTTAAGAAGTAATTTTAGTATTAAAGAGCAGCCA 2001  
GluGluAlaAlaGluLeuIleGluGluLeuValGlnLeuLysLys  
1940 1960 1962  
2002 AGGCTTTGTTGGTTTGTTGTTTTCATATACTTCCTGTCATTTTCTTTTCTTTTAATGTGTCAAGCGAC 2070  
2069  
2071 TCTGTTGGTTTAAAGTAGTATCTGTTTGGCCATGGATCTCTCTCTCTATTGTCGACTGAAAACTTTTGGTT 2139  
2082 2100 2104 2119 2120 2121  
2140 TACACATGAAAGCTT 2154  
2152 2150  
2150

DdeI  
AluI  
TaqI  
EcoRV  
SacI  
AluI  
AluI  
AluI  
DraI  
HindIII  
AluI  
HincII  
AccI  
Sau3AI  
NcoI  
TaqI  
Sali  
HincII  
AccI

FIGURE 3G

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Brassica Campestris Seed Specific cDNA-EA9

1 TTCAACTTTTCTAAACCAATGGCTTTTAAACACAGATCCAAATCTTTCTCATTTGTCTCTCTAGTCTCATC 69  
METAlaLeuThrGlnIleGlnIlePheLeuIleValSerLeuValSerSe  
34  
TaqI  
Sau3AI  
Clal  
70 ATTCAGTTTATCGATCAGTCTTTCTCGTCCATTACTCGATGAAGTCGCCCATGCAAAAGACACATGCCGA 138  
rPheSerLeuSerIleThrLeuSerArgProLeuLeuAspGluValAlaMETGlnLysArgHisAlaGl  
81 82 81 106  
HaeIII  
139 GTGGATGACCGAACACGGCCGTGTTTACGCAGATGCGAACGAGAAAAACAACCGCTACGCTGTTTCAA 207  
uTrpMETThrGluHisGlyArgValTyrAlaAspAlaAsnGluLysAsnArgTyrAlaValPheLy  
157

Complete nucleotide sequence of B. campestris cDNA EA9. The longest open reading frame is designated by three letter amino acid code. PolyA tails are evident at the end of the sequence and a potential polyadenylation signal is underlined.

FIGURE 4A

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208	ACGCAACGTGGAACCGCATTGAACGCTTAAATGACGTTCAATCCGGACTAACGTTTAAACTCGGGTGAA	276	
	sArgAsnValGluArgIleGluArgLeuAsnAspValGlnSerGlyLeuThrPheLysLeuAlaValAs	250	HpaII
		263	DraI
277	CCAGTTTGCTGATCTAAACCAACGAAGAATCCGTTCTATGTACACTGGTTTCAAGGAACTCTGTGTT	345	
	nGlnPheAlaAspLeuThrAsnGluGluPheArgSerMETTyThrGlyPheLysGlyAsnSerValLe	318	RsaI
		303	EcoRI
		287	Sau3AI
346	GTCTAGTCGAACCTAAACCAACGTCGTTTAGGTACCAACAAACGTTTCTTCTGATGCGTTGCCGTTTCTGT	414	
	uSerSerArgThrLysProThrSerPheArgTyrglnAsnValSerSerAspAlaLeuProValSerVa	405	HpaII
		380	RsaI
		378	KpnI
		353	TaqI
415	TGATTGGAGGAAGAAAGGAGCTGTGACTCCTATCAAGGATCAAGGCTTATGCGGATCTTGTGGCGGTT	483	
	lAspTrpArgLysLysGlyAlaValThrProIleLysAspGlnGlyLeuCysGlySerCysTrpAlaPh	468	Sau3AI
		452	AluI
		435	

FIGURE 4B

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PvuII  
AluI  
|  
484 TTCAGCTGTTGGCGCTATAGAGGAGTAGCACAGATAAAGAAAGGAAACTCATTTCTTTGTCTGAACA 552  
eSerAlaValAlaAlaIleGluGlyValAlaGlnIleLysLysGlyLysLeuIleSerLeuSerGluGly  
489  
489  
  
TaqI  
Sali  
HincII  
AluI AccI  
| | | |  
553 AGAGCTTGTCGACTGCGACACAAACGATGGTGGCTGCATGGCGGTTTGTGATGGATACAGCGTTTAACTA 621  
nGluLeuValAspCysAspThrAsnAspGlyGlyCysMETGlyGlyLeuMETAspThrAlaPheAsnTy  
557 562  
560  
561  
562  
  
622 CACAATAACTATTGGCGGCTTAACCTCTGAATCAATTAATCCTTATAAAGCACAAACGGCATTGCAA 690  
rThrIleThrIleGlyGlyLeuThrSerGluSerAsnTyProTyLysSerThrAsnGlyThrCysAs  
|  
HpaII  
691 CTTCAATAAAACTAAACAGATAGCAACTTCTATCAAAAGGTTTGTGAGGATGTCCCGGCTAACGATGAGAA 759  
nPheAsnLysThrLysGlnIleAlaThrSerIleLysGlyPheGluAspValProAlaAsnAspGluLy  
744

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FIGURE 4C

097 011 30 . 100000



760 ACCCTAATGAAGCAGTGGCACACACCCGGTTAGCATTTGAATAGCGGGAGGAGATATTGGTTTCCA 828  
sAlaLeuMETLysAlaValAlaHisHisProValSerIleGlyIleAlaGlyGlyAspIleGlyPheG1  
789 HpaII

829 ATTCTATTCTCGTCCGGTGTGTTTCAGCGGAGAAATGCACAATCATCTTGTATCACGGGGTAACCTGCGGTGG 897  
nPhETyrSerSerGlyValPheSerGlyGluCysThrThrHisLeuAspHisGlyValThrAlaValG1  
841 875 875 Sau3AI  
HpaII BclI

898 ATACGGCCGATCTAAAACGGATTAAAGTACTGGATCCTCAAGAATTATCATGGGGACCAAAATGGGGAGA 966  
yTyrGlyArgSerLysAsnGlyLeuLysTyrTrpIleLeuLysAsnSerTrpGlyProLysTrpGlyG1  
904 906 927 931 941 951 ScaI Sau3AI  
HaeIII RsaI BamHI EcoRI AvaII

967 ACGTGGATACATGAGGATCAAAAAAGATATCAAGCCTAAACACGGACAATGTGGTCTTGCCATGCAATGC 1035  
uArgGlyTyrMETArgIleLysLysAspIleLysProLysHisGlyGlnCysGlyLeuAlaMETAsnAl  
982 995 Sau3AI EcoRV

FIGURE 4D

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Rsai | HindIII  
 HpaII | AluI  
 1036 TTCGTACCCCACTATGTGAAAAAATCGGTTCAATATCCGGTTAAGCTTTAGAAATAAAATGCTGCTGTTGG 1104  
 aSerTyrProThrMET  
 1041 1073 1081  
 1079

1105 TTATAATTTAAGACTCTGTGTTGCCATGTAATTTGTGAAATGGTAAGTTTATGTGATGCCAAAAGATTTCATA 1173

1174 AAAAAAAAAAAAAA 1186

FIGURE 4E

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3H11 TTTTTTTGAGCAAAGGGCAACTCAGATATCCAAAGATGAATCCAACATATA 51  
3H11 GCTTACAGCTGGGAGAACATTGTCTAACTCTTCTGAAATTTAAATGTTATC 102  
3H11 CAGAATCCTTCATCATAAAATAATATCAAAATGCAAATCTATTTTTTCTAC 153  
3H11 TCTTGTCTAGCTTCAACTTTCTTCTTCTGCTCATCAATTAGCAATTAATCC 204  
TGCTCATCAATTAGCAATTAATCC  
3H11 AAAACCATTATGGCTGCCAAAAATTCAGAGATGAAGTTTGCTATCTTCTTC 255  
2A11 AAAACCATTATGGCTGCCAAAAATTCAGAGATGAAGTTTGCTATCTTCTTC  
METAlaAlaLysAsnSerGluMETLysPheAlaIlePhePhe  
3H11 GTTGTCTTTTGACGACCACCTTTAGTTGATATGTCTGGAATTTGAAAAATG 306  
2A11 GTTGTCTTTTGACGACCACCTTTAGTTGATATGTCTGGAATTTGAAAAATG  
ValValLeuLeuThrThrThrLeuValAspMETSerGlyIleSerLysMET  
3H11 CAAGTGATGGCTCTTCGAGACATACCCCCACAAGAAACATTGCTGAAAAATG 357  
2A11 CAAGTGATGGCTCTTCGAGACATACCCCCACAAGAAACATTGCTGAAAAATG  
GlnValMETAlaLeuArgAspIleProProGlnGluThrLeuLeuLysMET  
3H11 AAGCTACTTCCCACAAATATTTTGGGACTTTGTAACGAACCTTGCAGCTCA 408  
2A11 AAGCTACTTCCCACAAATATTTTGGGACTTTGTAACGAACCTTGCAGCTCA  
LysLeuLeuProThrAsnIleLeuGlyLeuCysAsnGluProCysSerSer  
3H11 AACTCTGATTGCATCGGAATTACCCTTTGCCAATTTTGTAAGGAGAAGACG 459  
2A11 AACTCTGATTGCATCGGAATTACCCTTTGCCAATTTTGTAAGGAGAAGACG  
AsnSerAspCysIleGlyIleThrLeuCysGlnPhyCysLysGluLysThr  
3H11 GACCAGTATGGTTTAAACATACCGTACATGCAACCTGTTGCCCTTGAACAATA 510  
2A11 GACCAGTATGGTTTAAACATACCGTACATGCAACCTGTTGCCCTTGAACAATA  
AspGlnTyrGlyLeuThrTyrArgThrCysAsnLeuLeuPro  
3H11 TCAATGATCTATCGATCGATCTATCTATCTATTTATCTGTCTCTGCGCGTA 561  
2A11 TCAATGATCTATCGATCGATCTATCTATCTATTTATCTGTCTCTGCGCGTA  
3H11 TAGTGTTGTCTGTACCTTTGGTGTGAAGAATATGAATAAAGGGATACATAT 612  
2A11 TAGTGTTGTCTGTACCTTTGGTGTGAAGAATGTGAATAAAGGGATACATAT  
3H11 ATCTAGATATATTCTAGGTAATGTCCTATTGTATTTAAAATTTGTAGCAAT 663  
2A11 ATCTAGATATATTCTAGGTAATGTCCTATTGTATTTAAAATTTGTAGCAAT  
3H11 GATTGTTTGAATAAAAAACATACCATGAGTGAAATAATTATCCACATTAAT 714  
2A11 GATTGTTTGAATAAAAAACATACCATGAGTGAAATAATTATTC  
3H11 TCACGTATTTATTTCACTTATGATACGTATTTTGTTCCTTTCGCGTAAAA 765  
3H11 AAAAAAAAAA 774

FIGURE 5

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(a)

2A11

PA1b

Chick pea  
inhibitorLima bean  
inhibitor $\alpha_1$ -antitrypsin

V	M	A	L	R	D	I	P	P	Q	E	T	L	L
V	C	S	P	F	D	I	P	P	C	G	S	P	L
V	C	T	-	K	S	I	P	P	-	-	-	Q	C
L	C	T	-	K	S	I	P	P	-	-	-	Q	C
L	G	A	I	P	M	S	I	P	P	E	V		

(b)

2A11

PA1b

Barley chloroform/  
methanol-soluble  
protein dWheat  $\alpha$ -amylase  
inhibitor 0.28

Wheat albumin

Millet bi-functional  
inhibitorCastor bean 2S  
small subunit

Napin small subunit

T	N	I	L	G	L	C	N	E	P	C	S	S	N	S	D	C	I
G	S	P	L	C	R	C	I	P	A	G	L	V	I	G	N	C	R
T	N	L	L	G	N	C	R	-	F	Y	L	V	Q	Q	T	C	A
V	S	A	L	T	G	C	R	-	A	M	V	K	L	Q	-	C	V
V	P	A	L	P	A	C	R	P	L	-	L	R	L	Q	-	C	N
N	N	P	L	D	S	C	R	W	Y	V	S	A	T	K	R	A	C
Q	Q	N	L	R	Q	C	Q	E	Y	I	K	Q	Q	V	S	G	Q
A	Q	N	L	R	A	C	Q	Q	W	L	N	K	Q	A	M	Q	S

FIGURE 6

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2A11 GENOMIC

CTCGAGCCCT TTAAAAAGTA TAGTCAATAT TTACGGTGAC CGTGAATTC TTAAATTATGA 60  
TATATAATTT AAAAGAAATC ATGATCACAT TCTACTGATG AGAACATGTG CTAATCAAGG 120  
GAAAACATGG ATGTGAAAAA TACTTTTGT TAAAAAGTAAA AAAAAATGTG AAATTTTGT 180  
AGTTATTAC TACCTATACA TTATTTGAGC ATGTGCAAAC TTACAAAATA CCTAATAGAA 240  
GATTTTCACC TGCCTGTATA TATGTAAAT TATTATAATG AACACTCTCA CATAAAATAA 300  
TTATCAGTAT ATACATTAACT ACTTGCCCTC CACAATGAAT TAAATAAAT GTAGAACATG 360  
ATCTACACTT CAATAAAACT AAGACCATAA AGAATAATTT CAAAATATAC ACATGTCAAC 420  
AATAAATTAT TTGCATATTA TATTAACTTA CTAAACAATC TTTACTTTTG AAATATAAAA 480  
ATAATCAAGT TATAAGTCTG CTCAAAAGTAA AGCACTTGTT AGACTCATCT GATTTTGAGA 540  
AGGTAAGCAA ATTGATGGTG CATAATAGTC ACAAGTAAAA TATAAATAG ATTTCATTAG 600  
TAAAAATTGTT TTTTACTTTC TTTATATATA ATTATCAATA TCCTTCAATG GTAGGTTAAT 660  
TATATTTGTTA ACTTCTTGTT GAATTAAAGC AATAAGACAA GAATATTAAA GATAAAAGAA 720  
CAATAAAAAAT AGAAAGACTA AGAGATAAGA GTTTTCTTAT TCTTCTTTCA ATAAGTATCA 780  
TCAGTGTAT ACAATATAAA TTTTGTGATT TTGATCTAT CTATTTTATA TGTATATAT 840  
AAGCATACAA AAGATCAGTC ATAAATATGA CTTTAATCAT GAAAATAATG AAAGAGATTA 900

FIGURE 7A

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960 TGAAGGCGTA AGGTTACTAG AATAATAGTC ATTAATAAAA GGGTTATCT TTATAATTGA  
1020 ATAATTGATG AAGTAATGGA GATAATTAGT GAGCATAAAT TTTTTTAAAA AAATGGACAT  
1080 TTACACTATA ATATTTTATA ACACTTTCCC TTAAACATCT AGGTATAAAT AATGAGTCTT  
1140 GTCAAAATCT TAGTAGGAAA AATTCTGTGA AATTTTTTTA GTGAAAACAA ATGATATATA  
1200 TATCTTGAAT ACTCATTATT TGTTGTCTCA TTAAAAATCT TATCTGACCT ATAAAAATAA  
1260 TTATTTGCTC AACTCAAAAT AGTTTTTCAT TCTAAAAATTA GTATAATTAT TAGTGAATAT  
1320 TTAATTAACA TAATTGTATA CTAAGGGCCC TATAAATTGG ATTCTTCTCA AAGAAAAATA  
1378 AAATCACCAC ACAACTTTCT TCTTCTGCTC ATCAATTAGC AATTAATCCA AAACCATT  
1426 ATG GCT GCC AAA AAT TCA GAG ATG AAG TTT GCT ATC TTC TTC GTT GTT  
MET Ala Ala Lys Asn Ser Glu MET Lys Phe Ala Ile Phe Phe Val Val  
1474 CTT TTG ACG ACC ACT TTA GGTTCAACAAC ACTTCTCCCT TATTTTGT  
Leu Leu Thr Thr Thr Leu  
1534 TCTTAATTTC TTGGAAGTCA TATGCATGTG TTGGGTATCA TGGTATATAT ATAAAGGAAA  
1594 ATATTTTCTT TAATTACTGG TTTTCTAATG TTGGGTAGGT AATCGGAAAT TATTATGAGA  
1654 TAATGAACTT GCAAAGTCAT TATTATATAA CTTTTTTTTT ATACTTTGAT TTAAGAAATTC  
1714 ATTTTCTCTCA TTTTATATATA ACTTATTTTT CAACAGAAAA TATTTTTCGA ACTATTCAAA  
1774 CACACCCCTAA GACATTACAT ATATATATAT ATACACCCCTC CGTTTATAT TACTTAATGC

FIGURE 7B

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CTATTGAGTT GGGCCACCCT TTAAGAATGA TTCAATTAGA GATATGTTTT ACTAAATTAA 1834  
CCTATGCTTT AAGACTCTAA ATTGGCTAT TACTATTTTA CGTTGTAATT TAATGACAAA 1894  
CATTTCATAA TGACTATAGT CTGAACCTAA TTAGACAGAC GTATCTATAG TTTGCTTACT 1954  
AATGATTCAAT AGCTATATAT TTGGAGAGGA GAGAGACAAA CGATATTAAAG AAAGGGAGGA 2014  
GAGAGGGGAG GTAAATCTGA AATAGAGAAG AGAAAGGCAA CCAATTTTGA TCATCTATCA 2074  
TACTTTTGGAT TATTATTTTT ATTATATGTA CGTTTACATT ACAGTTTTCG AATTCTTTACA 2134  
TTAATCTTAA TCATAATATA TACA GTT GAT ATG TCT GGA ATT TCG AAA ATG CAA 2188  
Val Asp MET Ser Gly Ile Ser Lys MET Gln  
GTG ATG GCT CTT CGA GAC ATA CCC CCA CAA GAA ACA TTG CTG AAA ATG 2236  
Val MET Ala Leu Arg Asp Ile Pro pro Gln Glu Thr Leu Lys MET  
AAG CTA CTT CCC ACA AAT ATT TTG GGA CTT TGT AAC GAA CCT TGC AGC 2284  
Lys Leu Leu Pro Thr Asn Ile Leu Gly Leu Cys Asn Glu Pro Cys Ser  
TCA AAC TCT GAT TGC ATC GGA ATT ACC CTT TGC CAA TTT TGT AAG GAG 2332  
Ser Asn Ser Asp Cys Ile Gly Ile Thr Leu Cys Gln Phe Cys Lys Glu  
AAG ACG GAC CAG TAT GGT TTA ACA TAC CGT ACA TGC AAC CTG TTG CCT 2390  
Lys Thr Asp Gln Tyr Gly Leu Thr Tyr Arg Thr Cys Asn Leu Leu Pro  
TGA ACAATATCAA TGATCTATCG ATCGATCTAT CTATCTATTT ATCTGTCTCT 2433  
GGCGGTATAG TGTGTCTCTGT ACCTTTGGTG TGAAGAATAT GAATAAAGGG ATACATATAT 2493  
CTAGATATAT TCTAGGTAAT GTCCTATTGT ATTAAAAATT TGTAGCAATG ATTGTTTGAA 2553

FIGURE 7C

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TAAAAACATA CCATGAGTGA AATAATTATT CCACATTAAT TCACGTATTT ATTTCACTTA 2613  
TGATACGTAT TTTTGTTCCT TTGCGGTAGA TTTTGTGATCC TTTTCCCTTT TGAATATATA 2673  
ACATTAAACA CAAATAATGT TTATTAAATT AAGTTAATAT TTTTATTTAG CTATTTATAT 2733  
TTTTATTGA AATCAAACTT GATAAATATT TATAAAGATA ATTAACAAGT AATGTGACAC 2793  
TAACACCATG TAATATTATC TTGTCGTTAT TTATGATAAT ATTTAAAAAT TATAATTTCA 2853  
GTTAAAAAAT TATTAAAAAA ACATACTTTT AAAAAGTGAG TTAGCCTCCG CTACCCACAT 2913  
ACTTATGAAT TGGACTAGTT GTTTTTTGAC CCACAAAAAG AATGGGCTAA TTAAACCTGA 2973  
CCTATCAAAT TTCAGAAATCT GCATAGATTA GTCCGAACGA AATGAGTCAG CCCGTATTGA 3033  
ACAAAAATATC AACAAAGGAG TTATGTAAAG ATGTTTAAAG AGGAAAAAAG ATTTCTAATA 3093  
CATATGGACT TTCAATATCC CAACTTTGTC TGGCGATCTG AACCTGCTT AGTTTGTGA 3153  
TCATTAACTT GTCTTGCTAT GTATTTAAGA TTTAAACITT ATATGTTTAA ACTTACAGAA 3213  
AATACATATA AATCTCTCAA GACTTGGCAA CATAATTAC TTTAGTACTT AAACACATG 3273  
AAAAATTTAA TATCCTTTTA ACATCTTTGA AGTGAATTAA ATTATCACA TCCGAGCCTA 3333  
CACCTTGGAC GTGGCCGGCA CTCAGAACC AGTGCCTGTC CCCAAGCTAA CCTCATCCT 3393  
GACTGACTAC AAGCGGAAGG CTAACCTAAG TATACAAAAAG CTTAAAACTG AATAAAATA 3453  
ACTTTACAAG GTTTTAACAC AAATGAACAA CTTTGAAGAA AATAATATAT TCAACTAGCC 3513

FIGURE 7D

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ATAAAATAGA CAACTTTAGT CTTTAAAACA TTTAATAAAA TAAATGCAAA ATATAGACTC 3573  
CTTAACTAAA CTGACTATCT ATGGAGCCTC TAATTGATAA AGATGGAAGT CCGGACAAGA 3633  
CCACGACATC CTGACTAAAC TGAGAAAGTAA ATAAAATCCC CCGGAAAAAA AGGAGCCTCA 3693  
CCATGGCTAA CTCGAACTCG GGGATATATC AATGAAGCTC CTGTTGATGA TCTTGAAGAC 3753  
ATGTCCTCTGC ATCATCAAAA AGATGCAGGC CAAATGGCTC AGTACGTAAA ATGTACGAGT 3813  
ATGTAAGGGA AATTCTAAAG TATAACATAA GCTTGATACT TGAATAAAAAG GAAACATACT 3873  
TACCTCTTTT CAACTCAACT CAAATTAAGA ATAAGATACT CAACTCAAAG ATTAGGTATT 3933  
CAACGCAAAT ATGGCACTCT ACTCAATGAA GTACAAATTA ACTCAGGATA CTCGACTTAA 3993  
GATACTCAAC TCCCGACACT CAACTGAACT CATTCAATA TAAAGCAGCT TAAAAACAAGT 4053  
TCAGTATAAA GTAAAGTTGT TTAAAAACAT GATGTCAACT CTGTGTGTAT AATAAGGGAT 4113  
ACAACATAAC TTTGAAATGT ATATAAAAAT ACAATTAACT GATGTATATA AAAATACATT 4173  
AATCTATGGG AGATTCTCTA ACCGACAACC ATCACTTAAG GGCTAAGATG ATGATATAGC 4233  
GATCTACCGC ACGCTGCCAT CGCATCTTAT ACCCGGCCAA AGGTATAAGA CCTGAACCTGC 4293  
CTAATGAATC CACTAATAAA CTGTTAAAAAG GAATCATCTA AAAAGTATGA CCCTTTTCTA 4353  
CCCATAGTGG CTAACATGGT TTATGGGGGC TGTGAGTTAT CTGAACCTCTC CCCCATATCG 4413

FIGURE 7E

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GTGCTCAATA	CTACTCCAAA	AAATATACTG	CTCTTATGTT	TAAAAACATA	CTGATTCTGT	4473
GGTTTGAAAT	TATTGCTTAA	AGCTTAGATT	TTTGAAAAGC	TCTCTTTTGA	AAATCGTAGT	4533
TTCCCTTTTTC	TTCTATTAAA	GCTAGACATA	GGCTATGTAG	AACTCTAGCT	TACCTTCCTT	4593
CTCAAAAGTT	TGAAAACATT	TGCTTAGATT	CTTAGGGACT	ACTTAGTTCC	CTTGTGGA	4653
TTC						4656

FIGURE 7F

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## PG GENOMIC

10	20	30	40	50	60
AAGCTTCTTA AAAAGGCAAA TTGATTAATT TGAAGTCAAA ATAATTAATT ATAACAGTGG					
70	80	90	100	110	120
TAAAGCACCT TAAGAAACCA TAGTTTGAAA GGTTACCAAT GCGCTATATA TTAATCAACT					
130	140	150	160	170	180
TGATAATATA AAAAAAATTT CAATTCGAAA AGGGCCTAAA ATATTCTCAA AGTATTCGAA					
190	200	210	220	230	240
ATGGTACAAA ACTACCATCC GTCCACCTAT TGA CTCCAAA ATAAAAATTAT TATCCACCTT					
250	260	270	280	290	300
TGAGTTTAAA ATTGACTACT TATATAACAA TTCTAAATTT AACTATTTT AATACTTTTA					
310	320	330	340	350	360
AAAATACATG GCGTTCAAAT ATTTAATATA ATTTAATTTA TGAATATCAT TTATAAACCA					
370	380	390	400	410	420
ACCAACTACC AACTCATTAA TCATTAAATC CCACCCAAAT TCTACTATCA AAATTGTCCT					
430	440	450	460	470	480
AAACACTACT AAAACAAGAC GAAATTGTTC GAGTCCGAAT CGAAGCACCA ATCTAATTTA					
490	500	510	520	530	540
GGTTGAGCCG CATATTTAGG AGGACACTTT CAATAGTATT TTTTTC AAGC ATGAATTTGA					
550	560	570	580	590	600
AATTTAAGAT TAATGGTAAA GAAGTAGTAC ATCCCGAATT AATTCATGCC TTTTTTAAAT					
610	620	630	640	650	660
ATAATTATAT AAATATTTAT GATTTGTTTT AAATATTAAA ACTTGAATAT ATTATTTTTT					
670	680	690	700	710	720
TAAAAATTAT CTATTAAGTA CCATCACATA ATTGAGACGA AGGAATAATT AAGATGAACA					
730	740	750	760	770	780
TAGTGTTTAA TTAGTAATGG ATGGGTAGTA AATTTATTTA TAAATTATAT CAATAAGTTA					
790	800	810	820	830	840
AATTATAACA AATATTTGAG CGCCATGTAT TTTAAAAAAT ATTAAATAGT TTGAATTTAA					

FIGURE 8A

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850	860	870	880	890	900
					*
AACCGTTAGA TAAATGGTCA ATTTTGAACC CAAAAGTGGG TGAGAAGGGT ATTTTAGAGC					
910	920	930	940	950	960
					*
CAATAGGRGG ATGAGAAGGA TATTTTGAAG CCAATATGTG ATGGATGAAG GATAATTTTG					
970	980	990	1000	1010	1020
					*
TATCATTTCT AATACTTTAA AGATATTTTA GGTCATTTTC CCTTCTTTAG TTTATAGACT					
1030	1040	1050	1060	1070	1080
					*
ATAGTGTTAG TTCATCGAAT ATCATCTATT ATTTCCGTCT TAAATTATTT TTTATTTTAT					
1090	1100	1110	1120	1130	1140
					*
AAATTTTTTA AAAATAAATT ATTTTTCCTA TTAACTTTTG ATTGTAATTA ATTTTAAAAA					
1150	1160	1170	1180	1190	1200
					*
ATTACCAACA TATAAATAAA ATTAATATTT AACAAAGAAT TGTAACATAA TATTTTTTTA					
1210	1220	1230	1240	1250	1260
					*
ATTATTCAAA ATAAATATTT TTAAACATCA TATAAAAGAA ATACGACAAA AAAATTGAGA					
1270	1280	1290	1300	1310	1320
					*
CGCGAGAAGA CAAGCCAGAC AAAAATGTCC AAGAACTCT TTCGTCTAAA TATCTCTCAT					
1330	1340	1350	1360	1370	1380
					*
CCAAACTAAT ATAATACCCA TTATAATTAA CCATATTGAC CAACTCAAAC CCCTTAAAT					
1390	1400	1410	1420	1430	1440
					*
CTATAAATAG ACAAACCCTT CCCATACCTC TTATCATAAA AAAAATAATA ATCTTTTCA					
1450	1460	1470	1480	1490	1500
					*
ATAGACAAGT TTAAAAACCA TACCATATAA CAATATATCA TGGTTATCCA AAGGAATAGT					
1510	1520	1530	1540	1550	1560
					*
ATTCTCCTTC TCATTATTAT TTTTGCTTCA TCAATTTCAA CTTGTAGAAG CAATGTTATT					
1570	1580	1590	1600	1610	1620
					*
GATGACAATT TATTCAAACA AGTTTATGAT AATATTCTTG AACAAGAATT TGCTCATGAT					
1630	1640	1650	1660	1670	1680
					*
TTTCAAGCTT ATCTTTCTTA TTTGAGCAA AATATTGAAA GCAACAATAA TATTGACAAG					

FIGURE 8B

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1690	1700	1710	1720	1730	1740
					*
GTTGATAAAA ATGGGATTAA AGTGATTAAT GTACTTAGCT TTGGAGCTAA GGGTGATGGA					
1750	1760	1770	1780	1790	1800
					*
AAAACATATG ATAATATTGT AAGTATTTAA ATATTGGAAT ATATTTGTGG GGATGAAAAAT					
1810	1820	1830	1840	1850	1860
					*
GATAGAGAAT ATAAGAATTA TTTGGAAGGA TGAAAAGTTA TATTTTATAA AGTAGAAAAT					
1870	1880	1890	1900	1910	1920
					*
TATTTTCTCG TTTTLAGTAA TTAAAGGTGA AAAATGAGTT TTCTCGTAAG CGAGGAAAGT					
1930	1940	1950	1960	1970	1980
					*
CATTTTCCAT GGAACGTAT TTTTTTTTTTA CTTTAAATAA CGTCATAGTA TTTGCTATAC					
1990	2000	2010	2020	2030	2040
					*
TCAAGAATAA GACACTATTA TTGATGTTTA GTGCTCGAAA AGAAATTGAT AGTAATTTTG					
2050	2060	2070	2080	2090	2100
					*
CTAATATAAC TATCAATTTC TTATATGTAT ATTTTCAAC CAAAATAACA AAGCGTAATC					
2110	2120	2130	2140	2150	2160
					*
CAATAAGTGG GCCTCTAGAA TAAAGAGTAA GTTCTATTAA TTCTTAACCT TATTTAATTT					
2170	2180	2190	2200		
TATGGAAACC TCGACAAAAC GACAATGCTC AACTTATATT CGAATTC					

FIGURE 8C

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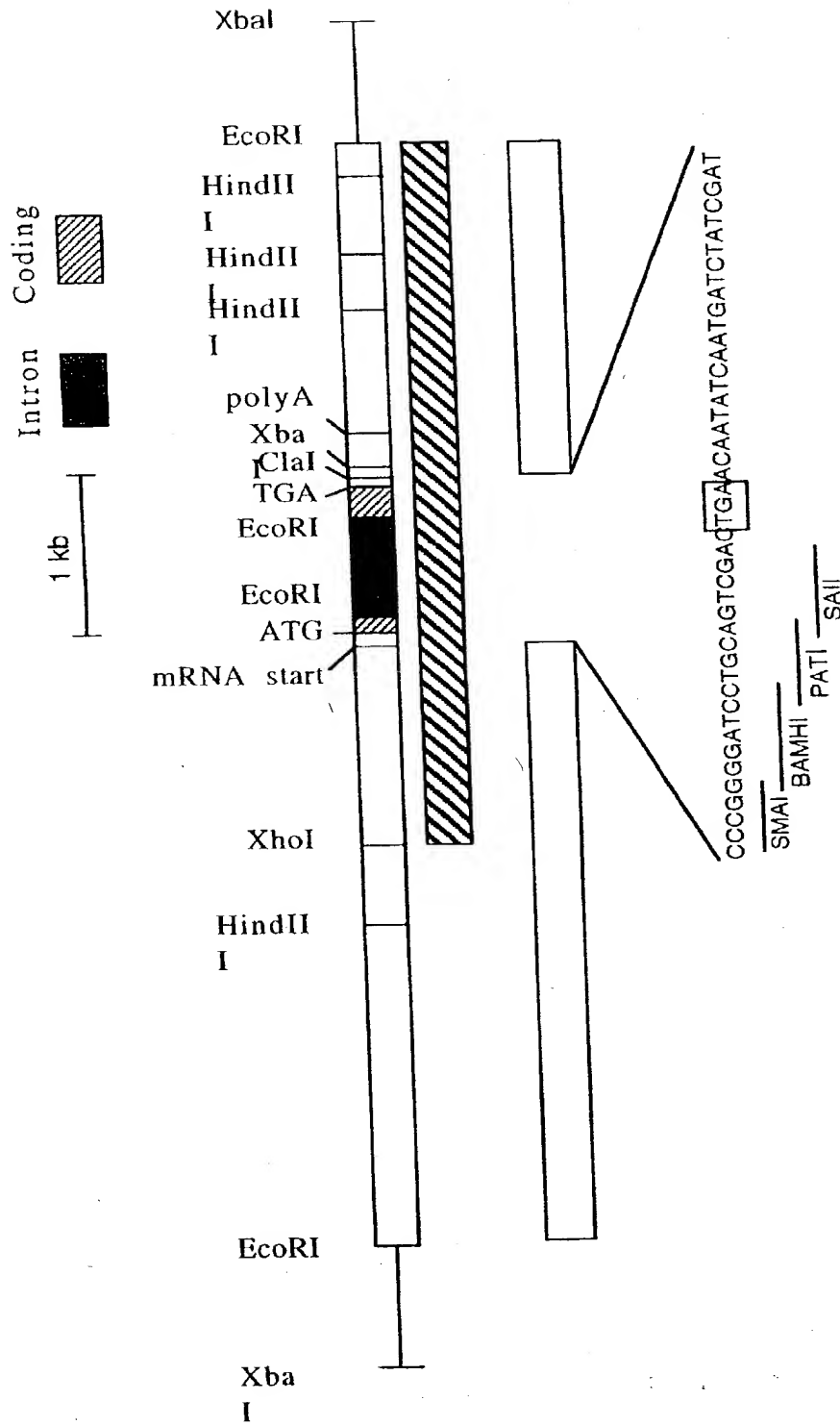


FIGURE 9

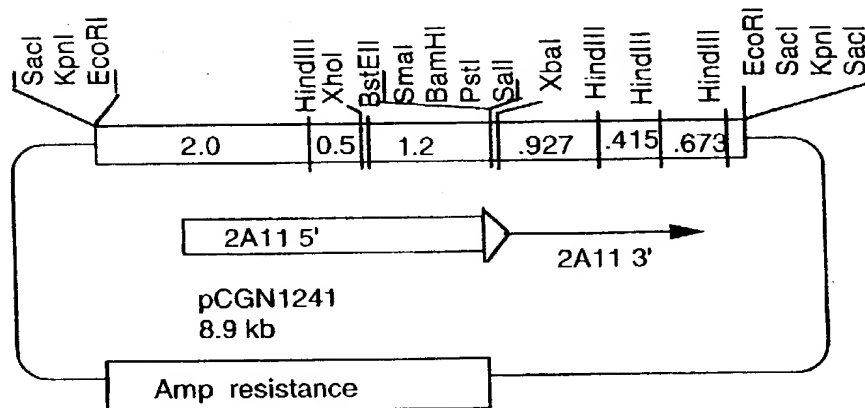
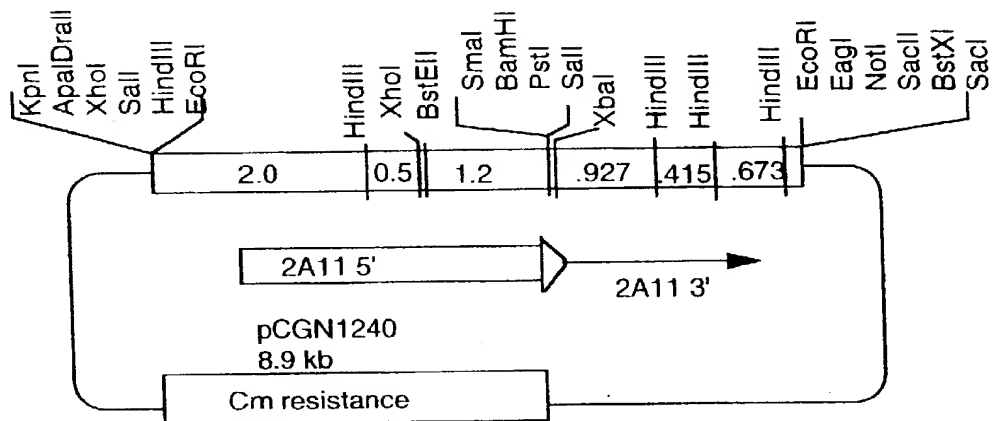


FIGURE 10A

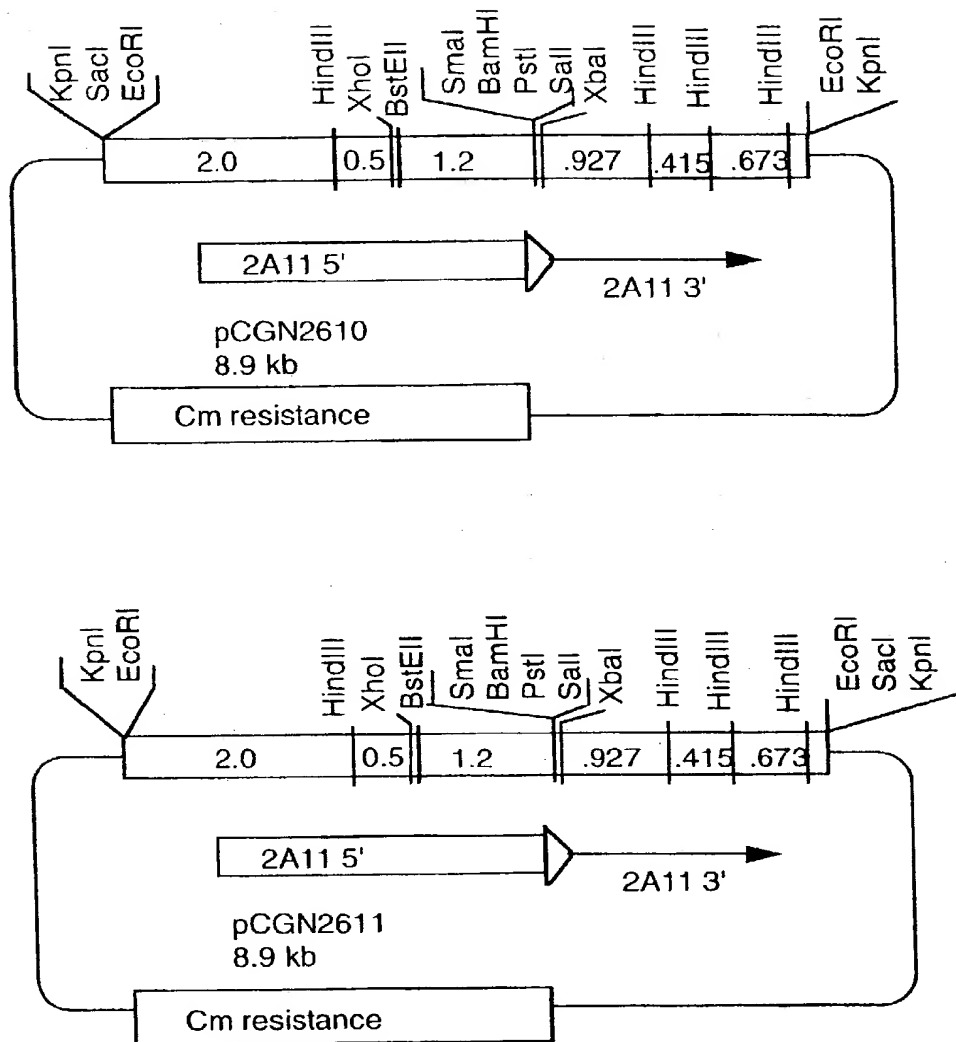


FIGURE 10B